

D. Steadman

#1118
RECEIVED Page 1 of 7
622-01

JUN 21 2001

TECH CENTER 1600/2900 1652

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/508,418

DATE: 05/21/2001
TIME: 09:50:59

Input Set : A:\Q58140.txt
Output Set: N:\CRF3\05212001\I508418.raw

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3 <110> APPLICANT: Nihon Nohyaku Co., Ltd.
5 <120> TITLE OF INVENTION: NOVEL PROTOPORPHYRINOGEN OXIDASE TOLERANT TO PHOTOBLEACHING HERBICIDE
7 <130> FILE REFERENCE: Q58140
9 <140> CURRENT APPLICATION NUMBER: 09/508,418
C--> 10 <141> CURRENT FILING DATE: 2000-06-08
12 <150> PRIOR APPLICATION NUMBER: JP 9-265084
13 <151> PRIOR FILING DATE: 1997-09-11
15 <160> NUMBER OF SEQ ID NOS: 11
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1874
21 <212> TYPE: DNA
22 <213> ORGANISM: Nicotiana tabacum
24 <220> FEATURE:
25 <221> NAME/KEY: exon
26 <222> LOCATION: (26)..(1672)
28 <220> FEATURE:
29 <221> NAME/KEY: misc_feature
30 <223> OTHER INFORMATION: Strain name: Xanthi NC
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36 1 5
38 cct aat att ttc act cac cag tcg tcg tca tcg cca ttg gca ttc tta 100
39 Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu
40 10 15 20 25
42 aac cgt acg agt ttc atc cct ttc tct tca atc tcc aag cgc aat agt 148
43 Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser
44 30 35 40
46 gtc aat tgc aat ggc tgg aga aca cga tgc tcc gtt gcc aaa gat tac 196
47 Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr
48 45 50 55
50 aca gtt cct tcc tca gcg gtc gac ggc gga ccc gcc gcg gag ctg gac 244
51 Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp
52 60 65 70
54 tgt gtt ata gtt gga gca gga att agt ggc ctc tgc att gcg cag gtg 292
55 Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val
56 75 80 85
58 atg tcc gct aat tac ccc aat ttg atg gta acc gag gcg aga gat cgt 340
59 Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg
60 90 95 100 105
62 gcc ggt ggc aac ata acg act gtg gaa aga gac ggc tat ttg tgg gaa 388
63 Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu
64 110 115 120
66 gaa ggt ccc aac agt ttc cag ccg tcc gat cct atg ttg act atg gca 436
67 Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala
68 125 130 135

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70 gta gat tgt gga ttg aag gat gat ttg gtg ttg gga gat cct aat gcg      484
71 Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala
72      140      145      150
74 ccc cgt ttc gtt ttg tgg aag ggt aaa tta agg ccc gtc ccc tca aaa      532
75 Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys
76      155      160      165
78 ctc act gat ctt ccc ttt ttt gat ttg atg agc att cct ggc aag ttg      580
79 Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu
80 170      175      180      185
82 aga gct ggt ttt ggt ccc att ggc ctc cgc cct tca cct cca ggt cat      628
83 Arg Ala Gly Phe Gly Pro Ile Gly Leu Arg Pro Ser Pro Pro Gly His
84      190      195      200
86 gag gaa tca gtt gag cag ttc gtg cgt cgt aat ctt ggt ggc gaa gtc      676
87 Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val
88      205      210      215
90 ttt gaa cgc ttg ata gaa cca ttt tgt tct ggt gtt tat gct ggt gat      724
91 Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp
92      220      225      230
94 ccc tca aaa ctg agt atg aaa gca gca ttt ggg aaa gtt tgg aag ttg      772
95 Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu
96      235      240      245
98 gaa gaa act ggt ggt agc att att gga gga acc ttt aaa gca ata aag      820
99 Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys
100 250      255      260      265
102 gag aga tcc agt aca cct aaa gcg ccc cgc gat ccg cgt tta cct aaa      868
103 Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys
104      270      275      280
106 cca aaa gga cag aca gtt gga tca ttc agg aag ggt ctc aga atg ctg      916
107 Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu
108      285      290      295
110 ccg gat gca atc agt gca aga ttg gga agc aaa tta aaa cta tca tgg      964
111 Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp
112      300      305      310
114 aag ctt tct agc att act aag tca gaa aaa gga gga tat cac ttg aca      1012
115 Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr
116      315      320      325
118 tac gag aca cca gaa gga gta gtt tct ctt caa agt cga agc att gtc      1060
119 Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val
120 330      335      340      345
122 atg act gtg cca tcc tat gta gca agc aac ata tta cgt cct ctt tcg      1108
123 Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser
124      350      355      360
126 gtt gcc gca gca gat gca ctt tca aat ttc tac tat ccc cca gtt gga      1156
127 Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly
128      365      370      375
130 gca gtc aca att tca tat cct caa gaa gct att cgt gat gag cgt ctg      1204
131 Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu
132      380      385      390
134 gtt gat ggt gaa cta aag gga ttt ggg cag ttg cat cca cgt aca cag      1252

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135 Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln
136      395      400      405
138 gga gtg gaa aca cta gga acg ata tat agt tca tca ctc ttc cct aac      1300
139 Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn
140 410      415      420      425
142 cgt gcc cca aaa ggt cgg gtg cta ctc ttg aac tac att gga gga gca      1348
143 Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala
144      430      435      440
146 aaa aat cct gaa att ttg tct aag acg gag agc caa ctt gtg gaa gta      1396
147 Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val
148      445      450      455
150 gtt gat cgt gac ctc aga aaa atg ctt ata aaa ccc aaa gct caa gat      1444
151 Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp
152      460      465      470
154 cct ctt gtt gtg ggt gtg cga gta tgg cca caa gct atc cca cag ttt      1492
155 Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe
156      475      480      485
158 ttg gtt ggt cat ctg gat acg cta agt act gca aaa gct gct atg aat      1540
159 Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn
160 490      495      500      505
162 gat aat ggg ctt gaa ggg ctg ttt ctt ggg ggt aat tat gtg tca ggt      1588
163 Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly
164      510      515      520
166 gta gca ttg ggg agg tgt gtt gaa ggt gct tat gaa gtt gca tcc gag      1636
167 Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu
168      525      530      535
170 gta aca gga ttt ctg tct cgg tat gca tac aaa tga aacctgtgtt      1682
171 Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys
172      540      545
174 ggggtagtc caaaccttgt tagtagtacg atcatgcctt gggaaaattg gcatgtgcct      1742
176 aaaagttttg ctcatagag ttattttagc cttggtaaat gatttgact tgatatcagt      1802
178 cgttttcttt gagataaaat gttcctgttc aggaaatata atgtatatca attttaaaca      1862
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184 <211> LENGTH: 548
185 <212> TYPE: PRT
186 <213> ORGANISM: Nicotiana tabacum
188 <220> FEATURE:
189 <221> NAME/KEY: misc_feature
190 <223> OTHER INFORMATION: Strain name: SR1
193 <400> SEQUENCE: 2
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198 Ser Ser Ser Ser Pro Leu Ala Phe Leu Asn Arg Thr Ser Phe Ile Pro
199      20      25      30
201 Phe Ser Ser Ile Ser Lys Arg Asn Ser Val Asn Cys Asn Gly Trp Arg
202      35      40      45
204 Thr Arg Cys Ser Val Ala Lys Asp Tyr Thr Val Pro Ser Ser Ala Val
205      50      55      60

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207 Asp Gly Gly Pro Ala Ala Glu Leu Asp Cys Val Ile Val Gly Ala Gly
208 65 70 75 80
210 Ile Ser Gly Leu Cys Ile Ala Gln Val Met Ser Ala Asn Tyr Pro Asn
211 85 90 95
213 Leu Met Val Thr Glu Ala Arg Asp Arg Ala Gly Gly Asn Ile Thr Thr
214 100 105 110
216 Val Glu Arg Asp Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln
217 115 120 125
219 Pro Ser Asp Pro Met Leu Thr Met Ala Val Asp Cys Gly Leu Lys Asp
220 130 135 140
222 Asp Leu Val Leu Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Lys
223 145 150 155 160
225 Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr Asp Leu Pro Phe Phe
226 165 170 175
228 Asp Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Phe Gly Pro Ile
229 180 185 190
231 Gly Leu Arg Pro Ser Pro Pro Gly His Glu Glu Ser Val Glu Gln Phe
232 195 200 205
234 Val Arg Arg Asn Leu Gly Gly Glu Val Phe Glu Arg Leu Ile Glu Pro
235 210 215 220
237 Phe Cys Ser Gly Val Tyr Val Gly Asp Pro Ser Lys Leu Ser Met Lys
238 225 230 235 240
240 Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Glu Thr Gly Gly Ser Ile
241 245 250 255
243 Ile Gly Gly Thr Phe Lys Ala Ile Lys Glu Arg Ser Ser Thr Pro Lys
244 260 265 270
246 Ala Pro Arg Asp Pro Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly
247 275 280 285
249 Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Asp Ala Ile Ser Ala Arg
250 290 295 300
252 Leu Gly Ser Lys Leu Lys Leu Ser Trp Lys Leu Ser Ser Ile Thr Lys
253 305 310 315 320
255 Ser Glu Lys Gly Gly Tyr His Leu Thr Tyr Glu Thr Pro Glu Gly Val
256 325 330 335
258 Val Ser Leu Gln Ser Arg Ser Ile Val Met Thr Val Pro Ser Tyr Val
259 340 345 350
261 Ala Ser Asn Ile Leu Arg Pro Leu Ser Val Ala Ala Ala Asp Ala Leu
262 355 360 365
264 Ser Asn Phe Tyr Tyr Pro Pro Val Gly Ala Val Thr Ile Ser Tyr Pro
265 370 375 380
267 Gln Glu Ala Ile Arg Asp Glu Arg Leu Val Asp Gly Glu Leu Lys Gly
268 385 390 395 400
270 Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val Glu Thr Leu Gly Thr
271 405 410 415
273 Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Lys Gly Arg Val
274 420 425 430
276 Leu Leu Leu Asn Tyr Ile Gly Gly Ala Lys Asn Pro Glu Ile Leu Ser
277 435 440 445
279 Lys Thr Glu Ser Gln Leu Val Glu Val Val Asp Arg Asp Leu Arg Lys

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280      450      455      460
282 Met Leu Ile Lys Pro Lys Ala Gln Asp Pro Leu Val Val Gly Val Arg
283 465      470      475      480
285 Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Thr
286      485      490      495
288 Leu Ser Thr Ala Lys Ala Ala Met Asn Asp Asn Gly Leu Glu Gly Leu
289      500      505      510
291 Phe Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val
292      515      520      525
294 Glu Gly Ala Tyr Glu Val Ala Ser Glu Val Thr Gly Phe Leu Ser Arg
295      530      535      540
297 Tyr Ala Tyr Lys
298 545
300 <210> SEQ ID NO: 3
301 <211> LENGTH: 1874
302 <212> TYPE: DNA
303 <213> ORGANISM: Nicotiana tabacum
305 <220> FEATURE:
306 <221> NAME/KEY: exon
307 <222> LOCATION: (26)..(1672)
309 <220> FEATURE:
310 <221> NAME/KEY: misc_feature
311 <223> OTHER INFORMATION: Strain name: SR1
314 <400> SEQUENCE: 3
315 agcgcggtct acaagtcagg cagtc atg aca aca act ccc atc gcc aat cat      52
316      Met Thr Thr Thr Pro Ile Ala Asn His
317      1      5
319 cct aat att ttc act cac cag tcg tcg tca tcg cca ttg gca ttc tta      100
320 Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu
321 10      15      20      25
323 aac cgt acg agt ttc atc cct ttc tct tca atc tcc aag cgc aat agt      148
324 Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser
325      30      35      40
327 gtc aat tgc aat ggc tgg aga aca cga tgc tcc gtt gcc aaa gat tac      196
328 Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr
329      45      50      55
331 aca gtt cct tcc tca gcg gtc gac ggc gga ccc gcc gcg gag ctg gac      244
332 Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp
333      60      65      70
335 tgt gtt ata gtt gga gca gga att agt ggc ctc tgc att gcg cag gtg      292
336 Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val
337      75      80      85
339 atg tcc gct aat tac ccc aat ttg atg gta acc gag gcg aga gat cgt      340
340 Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg
341 90      95      100      105
343 gcc ggt ggc aac ata acg act gtg gaa aga gac ggc tat ttg tgg gaa      388
344 Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu
345      110      115      120
347 gaa ggt ccc aac agt ttc cag ccg tcc gat cct atg ttg act atg gca      436

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/508,418

DATE: 05/21/2001

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